

SEQUENCE LISTING

<110> University of Utah Research Foundation
Adderson, Elisabeth
Bohnsack, John

<120> Isolated Genes for Virulent Group B Streptococcus agalactiae

<130> 1321.2.29

<150> 60/140,084
<151> 1999-06-21

<160> 10

<170> PatentIn version 3.0

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<212> DNA
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<221> CDS
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gg t at g c t g t a t c a c c a g t t a c g c c g a t a g c t t t t g c c g c t g a g a c a
Gly Met Ala Val Ser Pro Val Thr Pro Ile Ala Phe Ala Ala Glu Thr
          20           25           30

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ggg aca att aca gtt caa gat act caa aaa ggc gca acc tat aaa gca 144
 Gly Thr Ile Thr Val Gln Asp Thr Gln Lys Gly Ala Thr Tyr Lys Ala
 35 40 45

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tat aaa gtt ttt gat gca gaa ata gat aat gca aat gta tct gat tcg      192
Tyr Lys Val Phe Asp Ala Glu Ile Asp Asn Ala Asn Val Ser Asp Ser
      50           55           60

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aat aaa gat gga gct tct tat tta att cct caa ggt aaa gaa gct gag 240
Asn Lys Asp Gly Ala Ser Tyr Leu Ile Pro Gln Gly Lys Glu Ala Glu
65          70           75           80

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tat aaa gct tca act gat ttt aat tct ctt ttt acg aca act act aat 288
Tyr Lys Ala Ser Thr Asp Phe Asn Ser Leu Phe Thr Thr Thr Asn
85 90 95

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gga ggg aga aca tat gta act aaa aaa gat act gcg tca gca aat gag      336
Gly Gly Arg Thr Val Thr Lys Lys Asp Thr Ala Ser Ala Asn Glu
          100           105           110

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att gcg aca tgg gct aaa tct ata tca gct aat act aca cca gtt tcc 384
 Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala Asn Thr Thr Pro Val Ser

115	120	125	
act gtt act gag tca aat aat gat ggt act gag gtt att aat gtt tcc Thr Val Thr Glu Ser Asn Asn Asp Gly Thr Glu Val Ile Asn Val Ser			432
130	135	140	
caa tat gga tat tat tat gtt tct agc act gtt aat aat gga gct gta Gln Tyr Gly Tyr Tyr Val Ser Ser Thr Val Asn Asn Gly Ala Val			480
145	150	155	160
att atg gtt aca tct gta act cca aat gct act att cat gaa aag aat Ile Met Val Thr Ser Val Thr Pro Asn Ala Thr Ile His Glu Lys Asn			528
165	170	175	
act gat gcg aca tgg gga gat ggt ggt gga aaa act gta gat caa aaa Thr Asp Ala Thr Trp Gly Asp Gly Gly Lys Thr Val Asp Gln Lys			576
180	185	190	
acg tac tcg gtt ggt gat aca gtc aaa tat act att act tat aag aat Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr Thr Ile Thr Tyr Lys Asn			624
195	200	205	
gca gtc aat tat cat ggt aca gaa aaa gtg tat caa tat gtt ata aag Ala Val Asn Tyr His Gly Thr Glu Lys Val Tyr Gln Tyr Val Ile Lys			672
210	215	220	
gat act atg cca tct gct tct gta gtt gat ttg aac gaa ggg tct tat Asp Thr Met Pro Ser Ala Ser Val Val Asp Leu Asn Glu Gly Ser Tyr			720
225	230	235	240
gaa gta act att act gat gga tca ggg aat att aca act cta act caa Glu Val Thr Ile Thr Asp Gly Ser Gly Asn Ile Thr Thr Leu Thr Gln			768
245	250	255	
ggt tcg gaa aaa gca act ggg aag tat aac ctg tta gag gaa aat aat Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn Leu Leu Glu Glu Asn Asn			816
260	265	270	
aat ttc acg att act att ccg tgg gca gct acc aat act cca acc gga Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala Thr Asn Thr Pro Thr Gly			864
275	280	285	
aat act caa aat gga gct aat gat gac ttt ttt tat aag gga ata aat Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe Phe Tyr Lys Gly Ile Asn			912
290	295	300	
aca atc aca gtc act tat aca gga gta tta aag agt gga gct aaa cca Thr Ile Thr Val Thr Tyr Thr Gly Val Leu Lys Ser Gly Ala Lys Pro			960
305	310	315	320
ggt tca gct gat tta cca gaa aat aca aac att gcg acc atc aac ccc Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn Ile Ala Thr Ile Asn Pro			1008
325	330	335	
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<212> PRT
<213> Streptococcus agalactiae

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Tyr Lys Val Phe Asp Ala Glu Ile Asp Asn Ala Asn Val Ser Asp Ser
50 55 60

Asn Lys Asp Gly Ala Ser Tyr Leu Ile Pro Gln Gly Lys Glu Ala Glu
65 70 75 80

Tyr Lys Ala Ser Thr Asp Phe Asn Ser Leu Phe Thr Thr Thr Asn
85 90 95

Gly Gly Arg Thr Tyr Val Thr Lys Lys Asp Thr Ala Ser Ala Asn Glu
100 105 110

Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala Asn Thr Thr Pro Val Ser
115 120 125

Thr Val Thr Glu Ser Asn Asn Asp Gly Thr Glu Val Ile Asn Val Ser
130 135 140

Gln Tyr Gly Tyr Tyr Val Ser Ser Thr Val Asn Asn Gly Ala Val
145 150 155 160

Ile Met Val Thr Ser Val Thr Pro Asn Ala Thr Ile His Glu Lys Asn
165 170 175

Thr Asp Ala Thr Trp Gly Asp Gly Gly Lys Thr Val Asp Gln Lys
180 185 190

Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr Thr Ile Thr Tyr Lys Asn
195 200 205

Ala Val Asn Tyr His Gly Thr Glu Lys Val Tyr Gln Tyr Val Ile Lys
210 215 220

Asp Thr Met Pro Ser Ala Ser Val Val Asp Leu Asn Glu Gly Ser Tyr
225 230 235 240

Glu Val Thr Ile Thr Asp Gly Ser Gly Asn Ile Thr Thr Leu Thr Gln
245 250 255

Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn Leu Leu Glu Asn Asn

260

265

270

Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala Thr Asn Thr Pro Thr Gly
275 280 285

Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe Phe Tyr Lys Gly Ile Asn
290 295 300

Thr Ile Thr Val Thr Tyr Thr Gly Val Leu Lys Ser Gly Ala Lys Pro
305 310 315 320

Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn Ile Ala Thr Ile Asn Pro
325 330 335

Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys Val Thr Val Arg Asp Gly
340 345 350

Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser Thr Lys Ala Ser Leu Gln
355 360 365

Gly Ala Ile Phe Val Leu Lys Asn Ala Thr Gly Gln Phe Leu Asn Phe
370 375 380

Asn Asp Thr Asn Asn Val Glu Trp Gly Thr Glu Ala Asn Ala Thr Glu
385 390 395 400

Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile Thr Gly Leu Lys Glu
405 410 415

Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala Pro Leu Gly Tyr Asn Leu
420 425 430

Leu Asp Asn Ser Gln Lys Val Ile Leu Gly Asp Gly Ala Thr Asp Thr
435 440 445

Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu Asn Asn Lys
450 455 460

Gly Thr Glu Leu Pro Ser Thr Gly Gly Ile Gly Thr Thr Ile Phe Tyr
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Arg Arg Arg Leu Arg Ser
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<222> (1) .. (1692)

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1 5 10 15				
att ata tcc aag atc ctt cag gta cat att att ata agt atg att cac				96
Ile Ile Ser Lys Ile Leu Gln Val His Ile Ile Ile Ser Met Ile His				
20 25 30				
gag ata aag atc ccg actcaa cta aag atg cct att ata cga cag ata				144
Glu Ile Lys Ile Pro Thr Gln Leu Lys Met Pro Ile Ile Arg Gln Ile				
35 40 45				
cta gtc tca tca aat gtt gat aca aca act aag tac aag tac gta aaa				
Leu Val Ser Ser Asn Val Asp Thr Thr Thr Lys Tyr Lys Tyr Val Lys				
50 55 60				
gac gct tac aaa tta gtc ggt tgg tat tat gtt aat cca tat ggt agt				240
Asp Ala Tyr Lys Leu Val Gly Trp Tyr Tyr Val Asn Pro Tyr Gly Ser				
65 70 75 80				
att aga cct tat aac ttt tca ggt gct gta act caa gat atc aat tta				
Ile Arg Pro Tyr Asn Phe Ser Gly Ala Val Thr Gln Asp Ile Asn Leu				
85 90 95				
aga gct att tgg cga aag gct gga gat tat cat att ata tac agc aat				336
Arg Ala Ile Trp Arg Lys Ala Gly Asp Tyr His Ile Ile Tyr Ser Asn				
100 105 110				
gat gct gtt ggt aca gat gga aag cca gca ttg gat gct tct ggt cag				
Asp Ala Val Gly Thr Asp Gly Lys Pro Ala Leu Asp Ala Ser Gly Gln				
115 120 125				
caa tta caa aca agt aat gag cct act gac cct gat tcc tat gac gat				
Gln Leu Gln Thr Ser Asn Glu Pro Thr Asp Pro Asp Ser Tyr Asp Asp				
130 135 140				
ggc tcc cat tca gcc tta ctg aga cgt ccg aca atg cca gat ggc tat				480
Gly Ser His Ser Ala Leu Leu Arg Arg Pro Thr Met Pro Asp Gly Tyr				
145 150 155 160				
cgt ttc cgt ggc tgg tgg tac aat ggt aaa att tat aac cca tat gat				
528				

Arg Phe Arg Gly Trp Trp Tyr Asn Gly Lys Ile Tyr Asn Pro Tyr Asp			
165	170	175	
tcc att gat att gac gcc cat tta gca gat gct aat aaa aat atc acc			576
Ser Ile Asp Ile Asp Ala His Leu Ala Asp Ala Asn Lys Asn Ile Thr			
180	185	190	
ata aaa cct gtc att att cca gta gga gat atc aaa tta gaa gat acc			624
Ile Lys Pro Val Ile Ile Pro Val Gly Asp Ile Lys Leu Glu Asp Thr			
195	200	205	
tcc atc aaa tac aat ggt aac ggt ggt act aga gta gaa aat ggt aat			672
Ser Ile Lys Tyr Asn Gly Asn Gly Gly Thr Arg Val Glu Asn Gly Asn			
210	215	220	
gtg gta aca caa gtg gag aca ccg cgt atg gag ttg aat agc aca act			720
Val Val Thr Gln Val Glu Thr Pro Arg Met Glu Leu Asn Ser Thr Thr			
225	230	235	240
aca att cct gaa aac caa tac ttt aca agg aca ggt tac aac ctt att			768
Thr Ile Pro Glu Asn Gln Tyr Phe Thr Arg Thr Gly Tyr Asn Leu Ile			
245	250	255	
ggg tgg cat cat gat aag gat tta gct gat aca gga cgt gtg gaa ttt			816
Gly Trp His His Asp Lys Asp Leu Ala Asp Thr Gly Arg Val Glu Phe			
260	265	270	
aca gca ggt caa tca ata ggt att gat aac aac ctt gat gca aca aat			864
Thr Ala Gly Gln Ser Ile Gly Ile Asp Asn Asn Leu Asp Ala Thr Asn			
275	280	285	
acc tta tat gct gtt tgg caa cct aaa gaa tac acc gtc gga gta agt			912
Thr Leu Tyr Ala Val Trp Gln Pro Lys Glu Tyr Thr Val Gly Val Ser			
290	295	300	
aaa act gtc gtt gga cta gat gaa gat aag acg aaa gac ttc ttg ttt			960
Lys Thr Val Val Gly Leu Asp Glu Asp Lys Thr Lys Asp Phe Leu Phe			
305	310	315	320
aat cca agt gaa acg ttg caa caa gag aat ttt ccg ctg aga gat ggt			1008
Asn Pro Ser Glu Thr Leu Gln Gln Glu Asn Phe Pro Leu Arg Asp Gly			
325	330	335	
cag act aag gaa ttt aaa gta cct tat gga act tct ata tca ata gat			1056
Gln Thr Lys Glu Phe Lys Val Pro Tyr Gly Thr Ser Ile Ser Ile Asp			
340	345	350	
gaa caa gcc tac gat gaa ttt aaa gta tct gag tca att aca gaa aaa			1104
Glu Gln Ala Tyr Asp Glu Phe Lys Val Ser Glu Ser Ile Thr Glu Lys			
355	360	365	
aat cta gca act ggt gaa gct gat aaa act tat gat gct acc ggc tta			1152
Asn Leu Ala Thr Gly Glu Ala Asp Lys Thr Tyr Asp Ala Thr Gly Leu			
370	375	380	
caa tcc ctg aca gtt tca gga gac gta gat att agc ttt acc aat aca			1200
Gln Ser Leu Thr Val Ser Gly Asp Val Asp Ile Ser Phe Thr Asn Thr			

385	390	395	400	
cgt atc aag caa aaa gta cga cta cag aaa gtt aat gtc gaa aat gat Arg Ile Lys Gln Lys Val Arg Leu Gln Lys Val Asn Val Glu Asn Asp 405		410		1248
aat aat ttt tta gca ggt gca gtt ttt gat att tat gaa tca gat gct Asn Asn Phe Leu Ala Gly Ala Val Phe Asp Ile Tyr Glu Ser Asp Ala 420		425		1296
aat ggg aat aaa gct tca cat cct atg tat tca ggg ctg gtg aca aac Asn Gly Asn Lys Ala Ser His Pro Met Tyr Ser Gly Leu Val Thr Asn 435		440		1344
gat aaa ggc ttg tta tta gtg gat gct aat aac tac ctc agt ttg cca Asp Lys Gly Leu Leu Val Asp Ala Asn Asn Tyr Leu Ser Leu Pro 450		455		1392
gta gga aaa tac tac cta aca gag aca aag gcc cct cca ggg tac cta Val Gly Lys Tyr Tyr Leu Thr Glu Thr Lys Ala Pro Pro Gly Tyr Leu 465		470		1440
cta cct aaa aat gat gat ata tca gta tta gtg att tct acg gga gtt Leu Pro Lys Asn Asp Asp Ile Ser Val Leu Val Ile Ser Thr Gly Val 485		490		1488
acc ttt gaa caa aat ggt aat aat gcg aca cca ata aaa gag aat tta Thr Phe Glu Gln Asn Gly Asn Asn Ala Thr Pro Ile Lys Glu Asn Leu 500		505		1536
gtg gat gga agt aca gta tat act ttt aaa att act aac agt aaa gga Val Asp Gly Ser Thr Val Tyr Thr Phe Lys Ile Thr Asn Ser Lys Gly 515		520		1584
aca gaa ttg cct agt act gga ggt att gga aca cac att tat atc cta Thr Glu Leu Pro Ser Thr Gly Gly Ile Gly Thr His Ile Tyr Ile Leu 530		535		1632
gtt ggt tta gct tta gct cta cca tca gga tta ata tta tac tat cga Val Gly Leu Ala Leu Ala Leu Pro Ser Gly Leu Ile Leu Tyr Tyr Arg 545		550		1680
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 <213> Streptococcus agalactiae

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Glu Ile Lys Ile Pro Thr Gln Leu Lys Met Pro Ile Ile Arg Gln Ile
35 40 45

Leu Val Ser Ser Asn Val Asp Thr Thr Thr Lys Tyr Lys Tyr Val Lys
50 55 60

Asp Ala Tyr Lys Leu Val Gly Trp Tyr Tyr Val Asn Pro Tyr Gly Ser
65 70 75 80

Ile Arg Pro Tyr Asn Phe Ser Gly Ala Val Thr Gln Asp Ile Asn Leu
85 90 95

Arg Ala Ile Trp Arg Lys Ala Gly Asp Tyr His Ile Ile Tyr Ser Asn
100 105 110

Asp Ala Val Gly Thr Asp Gly Lys Pro Ala Leu Asp Ala Ser Gly Gln
115 120 125

Gln Leu Gln Thr Ser Asn Glu Pro Thr Asp Pro Asp Ser Tyr Asp Asp
130 135 140

Gly Ser His Ser Ala Leu Leu Arg Arg Pro Thr Met Pro Asp Gly Tyr
145 150 155 160

Arg Phe Arg Gly Trp Trp Tyr Asn Gly Lys Ile Tyr Asn Pro Tyr Asp
165 170 175

Ser Ile Asp Ile Asp Ala His Leu Ala Asp Ala Asn Lys Asn Ile Thr
180 185 190

Ile Lys Pro Val Ile Ile Pro Val Gly Asp Ile Lys Leu Glu Asp Thr
195 200 205

Ser Ile Lys Tyr Asn Gly Asn Gly Gly Thr Arg Val Glu Asn Gly Asn
210 215 220

Val Val Thr Gln Val Glu Thr Pro Arg Met Glu Leu Asn Ser Thr Thr
225 230 235 240

Thr Ile Pro Glu Asn Gln Tyr Phe Thr Arg Thr Gly Tyr Asn Leu Ile
245 250 255

Gly Trp His His Asp Lys Asp Leu Ala Asp Thr Gly Arg Val Glu Phe
260 265 270

Thr Ala Gly Gln Ser Ile Gly Ile Asp Asn Asn Leu Asp Ala Thr Asn
275 280 285

Thr Leu Tyr Ala Val Trp Gln Pro Lys Glu Tyr Thr Val Gly Val Ser
290 295 300

Lys Thr Val Val Gly Leu Asp Glu Asp Lys Thr Lys Asp Phe Leu Phe
305 310 315 320

Asn Pro Ser Glu Thr Leu Gln Gln Glu Asn Phe Pro Leu Arg Asp Gly
325 330 335

Gln Thr Lys Glu Phe Lys Val Pro Tyr Gly Thr Ser Ile Ser Ile Asp
340 345 350

Glu Gln Ala Tyr Asp Glu Phe Lys Val Ser Glu Ser Ile Thr Glu Lys
355 360 365

Asn Leu Ala Thr Gly Glu Ala Asp Lys Thr Tyr Asp Ala Thr Gly Leu
370 375 380

Gln Ser Leu Thr Val Ser Gly Asp Val Asp Ile Ser Phe Thr Asn Thr
385 390 395 400

Arg Ile Lys Gln Lys Val Arg Leu Gln Lys Val Asn Val Glu Asn Asp
405 410 415

Asn Asn Phe Leu Ala Gly Ala Val Phe Asp Ile Tyr Glu Ser Asp Ala
420 425 430

Asn Gly Asn Lys Ala Ser His Pro Met Tyr Ser Gly Leu Val Thr Asn
435 440 445

Asp Lys Gly Leu Leu Leu Val Asp Ala Asn Asn Tyr Leu Ser Leu Pro
450 455 460

Val Gly Lys Tyr Tyr Leu Thr Glu Thr Lys Ala Pro Pro Gly Tyr Leu

465 470 475 480

Leu Pro Lys Asn Asp Asp Ile Ser Val Leu Val Ile Ser Thr Gly Val
485 490 495

Thr Phe Glu Gln Asn Gly Asn Asn Ala Thr Pro Ile Lys Glu Asn Leu
500 505 510

Val Asp Gly Ser Thr Val Tyr Thr Phe Lys Ile Thr Asn Ser Lys Gly
515 520 525

Thr Glu Leu Pro Ser Thr Gly Gly Ile Gly Thr His Ile Tyr Ile Leu
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Val Gly Leu Ala Leu Ala Leu Pro Ser Gly Leu Ile Leu Tyr Tyr Arg
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Lys Lys Ile

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<210> 6
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<223> Synthetic oligonucleotide

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<210> 8
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<220>
<223> Synthetic oligonucleotide

<400> 8
cgattccctc g

11

<210> 9
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<223> Wherein X is any amino acid

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1 5

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1 5